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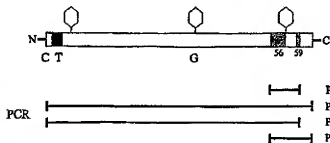
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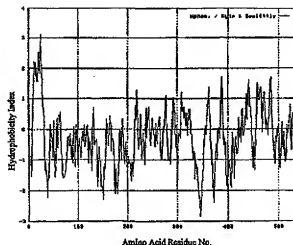
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(54) Title: BETA 1, 2-XYLOSYLTRANSFERASE-GENE FROM ARABIDOPSIS



(57) Abstract: A DNA molecule is provided which comprises a sequence according to SEQ ID NO: 8 having an open reading frame from base pair 227 to base pair 1831 or having at least 50 % homology to the above-indicated sequence, or hybridizing with the above-indicated sequence under stringent conditions, or comprising a sequence which has degenerated to the above-indicated DNA sequence because of the genetic code, the sequence coding for a plant protein having β 1,2-xylosyltransferase activity or being complementary thereto.



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BETA 1, 2-XYLOSYLTRANSFERASE-GENE FROM ARABIDOPSIS

The invention relates to polynucleotides coding for a β 1,2-xylosyltransferase. Furthermore, the invention relates to vectors comprising these polynucleotides, recombinant host cells, plants and insects transfected with the polynucleotides or with DNA derived therefrom, respectively, as well as to glycoproteins produced in these systems.

Glycoproteins exhibit a variety and complexity of carbohydrate units, the composition and arrangement of the carbohydrates being characteristic of different organisms. The oligosaccharide units of the glycoproteins have a number of tasks, e.g. they are important in regulating metabolism, they are involved in transmitting cell-cell interactions, they determine the circulation periods of proteins in circulation, and they are decisive for recognizing epitopes in antigen-antibody reactions.

The glycosylation of glycoproteins starts in the endoplasmatic reticulum (ER), where the oligosaccharides are either bound to asparagine side chains by N-glycosidic bonds or to serine or threonine side chains by O-glycosidic bonds. The N-bound oligosaccharides contain a common core from a penta-saccharide unit which consists of three mannose and two N-acetyl glucose amine residues. To modify the carbohydrate units further, the proteins are transported from the ER to the Golgi complex. The structure of the N-bound oligosaccharide units of glycoproteins is determined by their conformation and by the composition of the glycosyl transferases of the Golgi compartments in which they are processed.

It has been shown that the core pentasaccharide unit of the N-glycans of some plants is substituted by β 1,2-bound xylose and α 1,3-bound fucose (Lerouge et al., 1998, Plant Mol. Biol. 38, 31-48; Rayon et al., 1998, J. Exp. Bot. 49, 1463-1472). The heptasaccharide "MMXP³" constitutes the main oligosaccharide type in plants (Kurosaka et al., 1991, J. Biol. Chem., 266, 4168-4172; Wilson and Altmann, 1998, Glycoconj. J. 15, 1055-1070). These structures are also termed complex N-glycans or mannose-deficient

or truncated N-glycans, respectively. The α -mannosyl residues may be further replaced by GlcNAc, to which galactose and fucose are bound so that a structure is prepared which corresponds to the human Lewis a-epitope (Melo et al., 1997, FEBS Lett 415, 186-191; Fitchette-Laine et al., 1997, Plant J. 12, 1411-1417).

Neither β 1,2-xylose nor the α 1,3-bound fucose exist in mammalian glycoproteins. It has been found that the β 1,2-xylose together with α 1,3-fucose plays an important role in the epitope recognition of antibodies which are directed against plant N-bound oligosaccharides, and thereby trigger immune reactions in human or animal bodies against these oligosaccharides (Faye et al., 1993, Anal. Biochem. 209, 104-108). The β 1,2-xylose and/or α 1,3-fucose containing N-glycans furthermore seem to be one of the main causes for the wide-spread allergic cross reactivity between various plant and insect allergens and is also termed "cross-reactive carbohydrate determinant" (CCD). Due to the frequent occurrence of immunological cross reactions, the CCDs moreover mask allergy diagnoses.

The immunological reactions triggered in the human body by plant proteins are the main problem in the medicinal use of recombinant human proteins produced in plants. To circumvent this problem, β 1,2-xylosylation together with α 1,3-fucosylation would have to be prevented. According to a study, a mutant of the plant *Arabidopsis thaliana* was isolated in which the activity of N-acetylglucosaminyl transferase I, the first enzyme in the biosynthesis of complex glycans, is missing. The biosynthesis of the complex glycoproteins in this mutant thus is disturbed. Nevertheless, these mutant plants are capable of developing normally under certain conditions (A. Schaeven et al, 1993, Plant Physiol. 102; 1109-1118).

To block specifically the transfer of the β 1,2-xylose to an oligosaccharide without also interfering in other glycosylation steps, solely that enzyme would have to be inactivated which is directly responsible for this specific glycosylation, i.e. the β 1,2-xylosyltransferase. This transferase which only occurs in plants and some non-vertebrate animal species, e.g. in *Schistosoma* sp. (Khoo et al., 1997, Glycobiology 7, 663-677) and snail

(e.g. Mulder et al., 1995, Eur. J. Biochem. 232, 272-283), yet not in human beings or in other vertebrates, would have to be inactivated on purpose or suppressed so that human proteins which are produced in plants or in plant cells, respectively, would no longer contain this immune-reaction-triggering epitope, as has been the case so far.

β 1,2-xylosyltransferase transfers the D-xylose from UDP-xylose to the beta-linked mannose of plant N-linked oligosaccharides.

This enzyme was purified from soybean microsomes in 1997; Zeng et al.: J. Biol. Chem., 272, 31340-31347, 1997). According to this article, the best acceptor for xylose transfer was $\text{GlcNAc}_2\text{Man}_3\text{GlcNAc}_3\text{-T}$, but $\text{GlcNAc}_2\text{Man}_3\text{GlcNAc}_2$, with the GlcNAc on the 3-branch, was also a good acceptor. Furthermore, a number of other N-linked oligosaccharides were poor acceptors, especially those with galactose units at the nonreducing termini.

In the article by Rayon et al. (Plant Physiology, 1999, 119, 725-733) it is mentioned that Arabidopsis proteins are N-glycosylated by high-mannose-type N-glycans and by xylose- and fucose containing oligosaccharides. TEZUKA et al. (Eur. J. Biochem. 203, 401-413 (1992)) measured the activities of different enzymes, for example β 1,2-xylosyltransferase in the Golgi fraction of suspension-cultured cells of sycamore. They demonstrated that xylose was transferred onto the inner mannose by β 1,2-xylosyltransferase. Furthermore, they mentioned that xylose containing oligosaccharides are widely distributed throughout the plant kingdom although xylose containing N-linked oligosaccharides were also found in glycoproteins from gastropods and Chlorophyceae.

For the specific suppression or inactivation of proteins it is best to carry this out at the level of transcription and translation step, respectively. For this it is necessary to isolate and sequence the nucleotide sequence which codes for the active protein.

As mentioned above, the soybean β 1,2-xylosyltransferase was isolated and purified in 1997. Only a part of the xylosyltransferase cDNA has been isolated, s. WO99/29835 A1; SEQ ID NO 6 and 7),

however, the complete cDNA, which codes for the active protein could not be isolated and characterized so far. The reason why the nucleotide sequence has not been identified so far could be major problems in the procedure due to very low abundance of the mRNA which codes for the xylosyltransferase in the organisms, as for example soybeans. Until now, although several groups have tried to identify the entire nucleotide sequence of this gene, usually from soybeans, it was not possible to produce full length cDNA which corresponds to the xylosyltransferase mRNA with the help of conventional methods known to be effective in usual cases, for example with the help of the RACE-amplification (rapid amplification of cDNA ends). With this method unknown sequences are amplified with the help of specific amplification primers. Potential reasons for unsuccessful 5'-RACE experiments can be an inadequate choice of specific PCR primers as well as the presence of reverse transcriptase-inhibiting components during cDNA synthesis.

One problem of the isolated soybean β 1,2-xylosyl transferase is that its solubility and activity depends on the presence of detergents.

Additionally to the problem of the extremely low concentration of β 1,2-xylosyltransferase mRNA there is furthermore the problem that the secondary structure at the 5'-end of the RNA seems to hinder the amplification of this region. In these cases, the RACE amplification which is in itself a sensitive method, does not result in the correct and complete xylosyltransferase-cDNA sequence.

It is of course also very likely that the mRNA and the cDNA derived thereof, beside the fact that it is present only in very low concentrations, recombines and mutates very easily in the course of the various manipulations. For these and other potential reasons the cloning and the expression of this specific gene was impossible until now.

It is an object of the present invention to clone and to sequence the whole gene which codes for a plant β 1,2-xylosyltransferase, and to prepare vectors comprising this gene or an altered DNA or

a DNA derived therefrom, to transfect plants as well as cells thereof with one of these vectors, to produce glycoproteins that do not contain the normally occurring β 1,2-xylose, as well as to provide corresponding methods therefor.

A further object is the production of large quantities of purified recombinant enzyme in order to allow *in vitro* synthesis of homogenous N-glycans or glycoconjugates containing β 1,2-xylose. This will aid the further elucidation of the role of β 1,2-xylose in the immunogenicity and allergenicity of plant glycoproteins.

The object according to the invention is achieved by a DNA molecule comprising a sequence according to SEQ ID NO: 8 with an open reading frame from base pair 227 to base pair 1831 or being at least 50% homologous to the above sequence or hybridizing with the above-indicated sequence under stringent conditions, or comprising a sequence which has degenerated to the above DNA sequence due to the genetic code, the sequence coding for a plant protein which has β 1,2-xylosyltransferase activity or is complementary thereto. This complete sequence which has never been described is particularly useful for experiments, analysis and production processes which concern the β 1,2-xylosyltransferase activity. This sequence can be used especially for the inactivation or suppression of the β 1,2-xylosyltransferase as well as for overexpression and production of the recombinant enzyme.

Upon searching GenBank+EMBL+DDBJ+PDB databases using the soybean xylosyltransferase-derived peptides as mentioned above several polypeptide sequences (from *Arabidopsis* and *Drosophila*) with significant homologies were retrieved. However, these sequences were otherwise unrelated to each other as well as to the β 1,2-xylosyltransferase sequence finally identified. Successful retrieval of candidate sequence for β 1,2-xylosyltransferase was possible only by properly assembling three soybean β 1,2-xylosyl transferase-derived peptide sequences to a single sequence. All search strategies we used according to the present state of the art (i.e. using the peptide sequences separately or in combination with each other) did not lead to a successful retrieval of the correct sequence for β 1,2-xylosyltransferase.

The isolation and purification of this gene was achieved by searching in the DDBJ+GenBank+EMBL+PDB-databases corresponding sequences to three known peptides (used as assembled peptides) of the soybean xylosyltransferase (Patent WO99/29835 A1, SEQ ID NO: 3 and 5). It was found that one DNA sequence of *Arabidopsis thaliana* which has not yet been assigned to any protein before showed homology to two of the three peptides. With the help of the gene-finder program a predicted protein sequence was found according to which sequence specific primers for a RT-PCR were designed. It was possible to produce a first strand cDNA corresponding to the mRNA of the *A. thaliana*-xylosyltransferase gene after which the first strand cDNA was subjected to a PCR using the specifically designed primers. The reason for the successful production of *A. thaliana* xylosyltransferase-cDNA may be on the one hand that the xylosyltransferase-mRNA of *A. thaliana* is less problematic compared to other plant species, on the other hand the PCR was performed with optimally designed gene-specific primers.

The open reading frame of the SEQ ID NO: 8 codes for a protein with 534 amino acids and with a theoretical molecular weight of 60.2 kDa, a transmembrane portion presumably being present in the region between Ile11 and Phe29. The calculated pI value of the encoded protein of the sequence according to SEQ ID NO: 9 is 7.52.

The activity of the plant β 1,2-xylosyltransferase is detected by a method and measured, the xylosyltransferase being added to a sample containing UDP-xylose and a labelled acceptor (e.g. a glycopeptide or labelled oligosaccharide). After the reaction time, the content of bound xylose is measured. The activity of the xylosyltransferase in this case is seen as positive if the activity measurement is higher by at least 10 to 20%, in particular at least 30 to 50%, than the activity measurement of the negative control. The structure of the oligosaccharide may additionally be verified by means of HPLC. Such protocols are prior art (Staudacher et al., 1998, Anal. Biochem. 246, 96-101; Staudacher et al., 1991, Eur. J. Biochem. 199, 745-751). Whether the xylose is bound or not to the acceptor substrate can furthermore be determined by measuring the mass of the product by means of mass

spectrometry.

The pairing of two DNA molecules can be changed by selection of the temperature and ionic strength of the sample. By stringent conditions, according to the invention conditions are understood which allow for an exact, stringent, binding. For instance, the DNA molecules are hybridized in 7% sodium dodecyl sulfate (SDS), 0.5M NaPO₄, pH 7.0, 1mM EDTA at 50°C, and washed with 1% SDS at 42°C.

Whether sequences have an at least 50% homology to SEQ ID NO: 8 can be determined e.g. by means of the program FastDB of EMBL or SWISSPROT data bank.

There exist a number of relevant differences between recombinant β 1,2-xylosyltransferase encoded by the DNA molecule of the present invention and the respective enzyme from soybean as described in WO99/29835 A1:

1. The recombinant enzyme is soluble without detergents (e.g. Triton X-100), whereas the solubility of the enzyme from soybean depends on the presence of detergents.
2. The recombinant enzyme is fully active in the absence of detergents (e.g. Triton X-100).
3. The recombinant enzyme is N-glycosylated, whereas the enzyme from soybean is described to be unglycosylated.
4. The enzyme from *A. thaliana* exhibits full enzymatic activity also as a truncated form lacking the 32 N-terminal amino acids.
5. In contrast to the enzyme from soybean the enzyme from *A. thaliana* has a broad pH-optimum and shows pronounced activity in the range of pH 6 - 8.
6. The cDNA sequence coding for the soybean enzyme corresponds only to amino acids (aa) 199 - 469 of the *A. thaliana* protein, see figure 11.

7. The cDNA sequence coding for *A. thaliana* xylosyltransferase contains two insertions (corresponding to aa 375-382 and aa 425-429 of the predicted protein sequence) compared to the partial sequence of the soybean enzyme, see figure 11.

8. None of the five peptides (see figure 4 of WO99/29835 A1) isolated from the soybean enzyme is identical to the corresponding regions of the enzyme from *A. thaliana*:

Peptide SEQ ID NO. 1: homologous to aa 411-422 of the *A. thaliana* enzyme

Peptide SEQ ID NO. 2: homologous to aa 192-205 of the *A. thaliana* enzyme

Peptide SEQ ID NO. 3: homologous to aa 451-477 of the *A. thaliana* enzyme

Peptide SEQ ID NO. 4: homologous to aa 191-205 of the *A. thaliana* enzyme

Peptide SEQ ID NO. 5: homologous to aa 503-512 of the *A. thaliana* enzyme (remark: the cDNA sequence listed in WO99/29835 A1 does not contain a coding sequence for peptide 5).

Therefore the DNA molecule according to the present invention is particularly advantageous since it encodes for an active recombinant enzyme which shows surprisingly advantageous characteristics and effects over the known purified enzyme.

Preferably, the sequence of the DNA molecule of the invention encodes a protein with a β 1,2-xylosyltransferase activity. This specific protein is especially useful for analysis, experiments and production methods which relate to the β 1,2-xylosyltransferase.

Preferably, the DNA molecule according to the invention is at least 70%, preferably at least 80%, particularly preferred at least 95%, homologous with the sequence according to SEQ ID NO:

8. This sequence codes for a particularly active β 1,2-xylosyltransferase. The homology preferably is determined with a program which recognizes insertions and deletions and which does not consider these in the homology calculation.

According to a further advantageous embodiment, the DNA molecule comprises 1750 to 1850, in particular 1831, base pairs.

In doing so, it is particularly advantageous if one of the above-indicated DNA molecules is covalently associated with a detectable marker substance. As the marker (labelling) substance, any common marker can be used, such as, e.g., fluorescent, luminescent, radioactive markers, biotin, etc. In this manner, reagents are provided which are suitable for the detection, selection and quantitation of corresponding DNA molecules in solid tissue samples (e.g. from plants) or also in liquid samples, by means of hybridizing methods.

Preferably, the DNA molecule according to the invention includes a sequence which comprises a deletion, insertion and/or substitution mutation. The number of mutant nucleotides is variable and varies from a single one to several deleted, inserted or substituted nucleotides. It is also possible that the reading frame is shifted by the mutation. In such a "knock-out gene" it is merely important that the expression of a β 1,2-xylosyltransferase is disturbed, and the formation of an active, functional enzyme is prevented. In doing so, the site of the mutation is variable, as long as expression of an enzymatically active protein is prevented. Preferably, the mutation in the catalytic region of the enzyme which is located in the C-terminal region. The method of inserting mutations in DNA sequences are well known to the skilled artisan, and therefore the various possibilities of mutageneses need not be discussed here in detail. Coincidental mutageneses as well as, in particular, directed mutageneses, e.g. the site-directed mutagenesis, oligonucleotide-controlled mutagenesis or mutageneses by aid of restriction enzymes may be employed in this instance.

The invention further provides a DNA molecule which codes for a ribozyme which comprises two sequence sections, each of which has a length of at least 10 to 15 base pairs each, which are complementary to sequence sections of an inventive DNA molecule as described above so that the ribozyme complexes and cleaves the mRNA which is transcribed by a natural β 1,2-xylosyltransferase DNA mo-

lecle. The publication by John M. Burke "Clearing the way for ribozymes" (Nature Biotechnology 15:414-415; 1997) relates to the general mode of function of ribozymes. The ribozyme will recognize the mRNA of the β 1,2-xylosyltransferase by complementary base pairing with the mRNA. Subsequently, the ribozyme will cleave and destroy the RNA in a sequence-specific manner, before the enzyme is translated. After dissociation from the cleaved substrate, the ribozyme will repeatedly hybridize with RNA molecules and act as specific endonuclease. In general, ribozymes may specifically be produced for inactivation of a certain mRNA, even if not the entire DNA sequence which codes for the protein is known. Ribozymes are particularly efficient if the ribosomes move slowly along the mRNA. In that case it is easier for the ribozyme to find a ribosome-free site on the mRNA. For this reason, slow ribosome mutants are also suitable as a system for ribozymes (J. Burke, 1997, Nature Biotechnology; 15, 414-415).

One possible way is also to use a varied form of a ribozyme, i.e. a minizyme. Minizymes are efficient particularly for cleaving larger mRNA molecules. A minizyme is a hammer head ribozyme which has a short oligonucleotide linker instead of the stem/loop II. Dimer-minizymes are particularly efficient (Kuwabara et al., 1998, Nature Biotechnology, 16; 961-965).

A further aspect of the invention relates to a biologically functional vector which comprises one of the above-indicated DNA molecules. For transfection into host cells, an independent vector capable of amplification is necessary, wherein, depending on the host cell, transfection mechanism, task and size of the DNA molecule, a suitable vector can be used. Since a large number of different vectors is known, an enumeration thereof would go beyond the limits of the present application and there fore is done without here, particularly since the vectors are very well known to the skilled artisan (as regards the vectors as well as all the techniques and terms used in this specification which are known to the skilled artisan, cf. also Maniatis). Ideally, the vector has a small molecule mass and should comprise selectable genes so as to lead to an easily recognizable phenotype in a cell so thus enable an easy selection of vector-containing and vector-free host cells. To obtain a high yield of DNA and corresponding gene

products, the vector should comprise a strong promoter, as well as an enhancer, gene amplification signals and regulator sequences. For an autonomous replication of the vector, furthermore, a replication origin is important. Polyadenylation sites are responsible for correct processing of the mRNA and splice signals for the RNA transcripts. If phages, viruses or virus particles are used as the vectors, packaging signals will control the packaging of the vector DNA. For instance, for transcription in plants, Ti plasmids are suitable, and for transcription in insect cells, baculoviruses, and in insects, respectively, transposons, such as the P element.

If the above-described inventive vector is inserted into a plant or into a plant cell, a post-transcriptional suppression of the gene expression of the endogenous β 1,2-xylosyltransferase gene is attained by transcription of a transgene homologous thereto or of parts thereof, in sense orientation. For this sense technique, furthermore, reference is made to the publications by Baucombe 1996, Plant. Mol. Biol., 9:373-382, and Brigneti et al., 1998, EMBO J. 17:6739-6746. This strategy of "gene silencing" is an effective way of suppressing the expression of the β 1,2-xylosyltransferase gene, cf. also Waterhouse et al., 1998, Proc. Natl. Acad. Sci. USA, 95:13959-13964.

Furthermore, the invention relates to a biologically functional vector comprising a DNA molecule according to one of the above-described embodiments, being inversely orientated with respect to the promoter. If this vector is transfected in a host cell, an "antisense mRNA" will be read which is complementary to the mRNA of the β 1,2-xylosyltransferase and complexes the latter. This bond will either hinder correct processing, transportation, stability or, by preventing ribosome annealing, it will hinder translation and thus the normal gene expression of the β 1,2-xylosyltransferase.

Although the entire sequence of the DNA molecule could be inserted into the vector, partial sequences thereof because of their smaller size may be advantageous for certain purposes. With the antisense aspect, e.g., it is important that the DNA molecule is large enough to form a sufficiently large antisense mRNA which

will bind to the transferase mRNA. A suitable antisense RNA molecule comprises, e.g., from 50 to 200 nucleotides since many of the known, naturally occurring antisense RNA molecules comprise approximately 100 nucleotides.

For a particularly effective inhibition of the expression of an active β 1,2-xylosyltransferase, a combination of the sense technique and the antisense technique is suitable (Waterhouse et al., 1998, Proc. Natl. Acad. Sci., USA, 95:13959-13964).

Advantageously, rapidly hybridizing RNA molecules are used. The efficiency of antisense RNA molecules which have a size of more than 50 nucleotides will depend on the annealing kinetics *in vitro*. Thus, e.g., rapidly annealing antisense RNA molecules exhibit a greater inhibition of protein expression than slowly hybridizing RNA molecules (Wagner et al., 1994, Annu. Rev. Microbiol., 48:713-742; Rittner et al., 1993, Nucl. Acids Res., 21: 1381-1387). Such rapidly hybridizing antisense RNA molecules particularly comprise a large number of external bases (free ends and connecting sequences), a large number of structural subdomains (components) as well as a low degree of loops (Patzel et al. 1998; Nature Biotechnology, 16; 64-68). The hypothetical secondary structures of the antisense RNA molecule may, e.g., be determined by aid of a computer program, according to which a suitable antisense RNA DNA sequence is chosen.

Different sequence regions of the DNA molecule may be inserted into the vector. One possibility consists, e.g., in inserting into the vector only that part which is responsible for ribosome annealing. Blocking in this region of the mRNA will suffice to stop the entire translation. A particularly high efficiency of the antisense molecules also results for the 5'- and 3'-non translated regions of the gene.

The invention also relates to a biologically functional vector which comprises one of the two last-mentioned DNA molecules (mutation or ribozyme-DNA molecule). What has been said above regarding vectors also applies in this instance.

According to the invention, there is provided a method of prepa-

ring a cDNA comprising the DNA molecule of the invention, where in RNA is isolated from a plant cell, in particular from leaf cells, by means of which a reverse transcription is carried out after the addition of a reverse transcriptase and primers. The individual steps of this method are carried out according to protocols known per se. For the reverse transcription, on the one hand, it is possible to produce the cDNA of the entire mRNA with the help of oligo(dT) primers, and only then to carry out a PCR by means of selected primers so as to prepare DNA molecules comprising the β 1,2-xylosyltransferase gene. On the other hand, the selected primers may directly be used for the reverse transcription so as to obtain short, specific cDNA. The suitable primers may be prepared e.g. synthetically according to the pattern of cDNA sequences of the transferase.

The invention furthermore relates to a method of cloning a β 1,2-xylosyltransferase, characterized in that the DNA molecule of the invention is cloned into a vector which subsequently is transfected into a host cell or host, respectively, wherein, by selection and amplification of transfected host cells, cell lines are obtained which express the active β 1,2-xylosyltransferase. The DNA molecule is inserted into the vector by aid of restriction endonucleases, e.g.. For the vector, there applies what has already been said above. What is important in this method is that an efficient host-vector system is chosen. To obtain an active enzyme, eukaryotic host cells are particularly suitable. One possible way is to transfect the vector in insect cells. In doing so, in particular an insect virus would have to be used as vector, such as, e.g., baculovirus.

Of course, plants or plant cells, human or other vertebrate cells can also be transfected, in which case the latter would express an enzyme foreign to them.

Preferably, a method of preparing recombinant host cells, in particular plant cells or plants, respectively, with a suppressed or completely stopped β 1,2-xylosyltransferase production is provided, which is characterized in that at least one of the vectors according to the invention, i.e. that one comprising the inventive DNA molecule, the mutant DNA molecule or the DNA molecule

coding for ribozymes or the one comprising the DNA molecule in inverse orientation to the promoter, is inserted into the host cell or plant, respectively. What has been said above for the transfection also is applicable in this case.

As the host cells, plant cells may, e.g., be used, wherein, e.g., the Ti plasmid with the agrobacterium system is eligible. With the agrobacterium system it is possible to transfect a plant directly: agrobacteria cause root stem galls in plants. If agrobacteria infect an injured plant, the bacteria themselves do not get into the plant, but they insert the recombinant DNA portion, the so-called T-DNA, from the annular, extrachromosomal, tumour-inducing Ti-plasmid into the plant cells. The T-DNA, and thus also the DNA molecule inserted therein, are installed in the chromosomal DNA of the cell in a stable manner so that the genes of the T-DNA will be expressed in the plant.

There exist numerous known, efficient transfection mechanisms for different host systems. Some examples are electroporation, the calcium phosphate method, microinjection, liposome method.

Subsequently, the transfected cells are selected, e.g. on the basis of antibiotic resistences for which the vector comprises genes, or other marker genes. Then the transfected cell lines are amplified, either in small amounts, e.g. in Petri dishes, or in large amounts, e.g. in fermentors. Furthermore, plants have a particular characteristic, i.e. they are capable to re-develop from one (transfected) cell or from a protoplast, respectively, to a complete plant which can be grown.

Depending on the vector used, processes will occur in the host so that the enzyme expression will be suppressed or completely blocked:

If the vector comprising the DNA molecule with the deletion, insertion or substitution mutation is transfected, a homologous recombination will occur: the mutant DNA molecule will recognize the identical sequence in the genome of the host cell despite its mutation and will be inserted exactly on that place so that a "knock-out gene" is formed. In this manner, a mutation is intro-

duced into the gene for the β 1,2-xylosyltransferase which is capable of inhibiting the faultless expression of the β 1,2-xylosyltransferase. As has been explained above, with this technique it is important that the mutation suffices to block the expression of the active protein. After selection and amplification, the gene may be sequenced as an additional check so as to determine the success of the homologous recombination or the degree of mutation, respectively.

If the vector comprising the DNA molecule coding for a ribozyme is transfected, the active ribozyme will be expressed in the host cell. The ribozyme complexes the complementary mRNA sequence of the β 1,2-xylosyltransferase at least at a certain site, cleaves this site, and in this manner it can inhibit the translation of the enzyme. In this host cell as well as in cell lines, or optionally, plant, respectively, derived therefrom, β 1,2-xylosyltransferase will not be expressed.

In case the vector comprises the inventive DNA molecule in sense or inverse direction to the promoter, a sense or antisense-mRNA will be expressed in the transfected cell (or plant, respectively). The antisense mRNA is complementary at least to a part of the mRNA sequence of the β 1,2-xylosyltransferase and may likewise inhibit translation of the enzyme. As an example of a method of suppressing the expression of a gene by antisense technique, reference is made to the publication by Smith et al., 1990, Mol. Gen. Genet. 224:477-481, wherein in this publication the expression of a gene involved in the maturing process of tomatoes is inhibited. Double-stranded RNA (dsRNA) has recently been shown to trigger sequence-specific gene silencing in a wide variety of organisms, including nematodes, plants, trypanosomes, fruit flies and planaria; an as yet uncharacterized RNA trigger has been shown to induce DNA methylation in several different plant systems leading to selective interference with gene function (for review see Fire A., 1999, Trends Genet 15 (9): 358-363).

In all the systems, expression of the β 1,2-xylosyltransferase is at least suppressed, preferably even completely blocked. The degree of the disturbance of the gene expression will depend on the degree of complexing, homologous recombination, on possible sub-

sequent coincidental mutations and on other processes in the region of the genome. The transfected cells are checked for β 1,2-xylosyltransferase activity and selected.

Moreover, it is possible to still further increase the above-described suppression of the expression of the β 1,2-xylosyltransferase by introducing into the host a vector comprising a gene coding for a mammalian protein, e.g. β 1,4-galactosyltransferase, in addition to the insertion of an above-described vector. Xylosylation may be reduced by the action of other mammalian enzymes, the combination of the inhibition of the expression of an active β 1,2-xylosyltransferase by means of the inventive vector and by means of a mammalian enzyme vector being particularly efficient.

Any type of plant may be used for transfection, e.g. mung bean, tobacco plant, tomato and/or potato plant.

Another advantageous method of producing recombinant host cells, in particular plant cells, or plants, respectively, consists in that the DNA molecule comprising the mutation is inserted into the genome of the host cell, or plant, respectively, in the place of the non-mutated homologous sequence (Schaefer et al., 1997, Plant J.; 11(6):1195-1206). This method thus does not function with a vector, but with a pure DNA molecule. The DNA molecule is inserted into the host e.g. by gene bombardment, microinjection or electroporation, to mention just three examples. As has already been explained, the DNA molecule binds to the homologous sequence in the genome of the host so that a homologous recombination and thus reception of the deletion, insertion or substitution mutation, respectively, will result in the genome: Expression of the β 1,2-xylosyltransferase can be suppressed or completely blocked, respectively.

Preferably, recombinant plants or plant cells, respectively, are provided which have been prepared by one of the methods described above, their β 1,2-xylosyltransferase production being suppressed or completely blocked, respectively. Preferably, their β 1,2-xylosyltransferase activity is less than 50%, in particular less than 20%, particularly preferred 0%, of the β 1,2-xylosyltransferase activity occurring in natural plants or plant cells, respective-

ly. The advantage of these plants or plant cells, respectively, is that the glycoproteins produced by them do not comprise any or hardly comprise any β 1,2-bound xylose. If products of these plants are taken up by human or vertebrate bodies, there will be no immune reaction due to the β 1,2-xylose epitope.

The invention also relates to a PNA molecule comprising a base sequence complementary to the sequence of the DNA molecule according to the invention. PNA (peptide nucleic acid) is a DNA-like sequence, the nucleobases being bound to a pseudo-peptide backbone. PNA generally hybridizes with complementary DNA-, RNA- or PNA-oligomers by Watson-Crick base pairing and helix formation. The peptide backbone ensures a greater resistance to enzymatic degradation. The PNA molecule thus is an improved antisense agent.

Neither nucleases nor proteases are capable of attacking a PNA molecule. The stability of the PNA molecule, if bound to a complementary sequence, comprises a sufficient steric blocking of DNA and RNA polymerases, reverse transcriptase, telomerase and ribosomes. The publication by Pooga et al., "Cell penetrating PNA constructs regulate galanin receptor levels and modify pain transmission in vivo" (Nature Biotechnology 16:857-861; 1998) relates to PNA molecules in general and specifically to a PNA molecule that is complementary to human galanin receptor type 1 mRNA.

If the PNA molecule comprises the above-mentioned sequence, it will bind to the DNA or to a site of the DNA, respectively, which codes for β 1,2-xylosyltransferase and in this way is capable of inhibiting transcription of this enzyme. As it is neither transcribed nor translated, the PNA molecule will be prepared synthetically, e.g. by aid of the the t-Boc technique.

Advantageously, a PNA molecule is provided which comprises a base sequence which corresponds to the sequence of the inventive DNA molecule. This PNA molecule will complex the mRNA or a site of the mRNA of β 1,2-xylosyltransferase so that the translation of the enzyme will be inhibited. Similar arguments as set forth for the antisense RNA apply in this case. Thus, e.g., a particularly efficient complexing region is the translation start region or

also the 5'-non-translated regions of mRNA.

A further aspect of the present invention relates to a method of preparing plants or plant cells, respectively, in particular plant cells which comprise a blocked expression of the β 1,2-xylosyltransferase at the transcription or translation level, respectively, which is characterized in that inventive PNA molecules are inserted in the cells. To insert the PNA molecule or the PNA molecules, respectively, in the cell, again conventional methods, such as, e.g., electroporation or microinjection, are used. Particularly efficient is insertion if the PNA oligomers are bound to cell penetration peptides, e.g. transportan or pAntp (Pooga et al., 1998, Nature Biotechnology, 16; 857-861).

The invention provides a method of preparing recombinant glycoproteins which is characterized in that the inventive, recombinant plants or plant cells, respectively, whose β 1,2-xylosyltransferase production is suppressed or completely blocked, respectively, or plants or cells, respectively, in which the PNA molecules have been inserted according to the method of the invention, are transfected with the gene that expresses the glycoprotein so that the recombinant glycoproteins are expressed. In doing so, as has already been described above, vectors comprising genes for the desired proteins are transfected into the host or host cells, respectively, as has also already been described above. The transfected plant cells will express the desired proteins, and they have no or hardly any β 1,2-bound xylose. Thus, they do not trigger the immune reactions already mentioned above in the human or vertebrate body. Any proteins may be produced in these systems.

Advantageously, a method of preparing recombinant human glycoproteins is provided which is characterized in that the recombinant plants or plant cells, respectively, whose β 1,2-xylosyltransferase production is suppressed or completely blocked, or plants or cells, respectively, in which PNA molecules have been inserted according to the method of the invention, are transfected with the gene that expresses the glycoprotein so that the recombinant glycoproteins are expressed. By this method it becomes possible to produce human proteins in plants (plant cells) which, if taken

up by the human body, do not trigger any immune reaction directed against β 1,2-bound xylose residues. There, it is possible to utilize plant types for producing the recombinant glycoproteins which serve as food stuffs, e.g. banana, potato and/or tomato. The tissues of this plant comprise the recombinant glycoprotein so that, e.g. by extraction of the recombinant glycoprotein from the tissue and subsequent administration, or directly by eating the plant tissue, respectively, the recombinant glycoprotein is taken up in the human body.

Preferably, a method of preparing recombinant human glycoproteins for medical use is provided, wherein the inventive, recombinant plants or plant cells, respectively, whose β 1,2-xylosyltransferase production is suppressed or completely blocked, respectively, or plants or cells, respectively, into which the PNA molecules have been inserted according to the method of the invention, are transfected with the gene that expresses the glycoprotein so that the recombinant glycoproteins are expressed. In doing so, any protein can be used which is of medical interest.

Moreover, the present invention relates to recombinant glycoproteins according to a method described above, wherein they have been prepared in plant systems and wherein their peptide sequence comprises less than 50%, in particular less than 20%, particularly preferred 0%, of the β 1,2-bound xylose residues occurring in proteins expressed in non-xylosyltransferase-reduced plant systems. Naturally, glycoproteins which do not comprise β 1,2-bound xylose residues are to be preferred. The amount of β 1,2-bound xylose will depend on the degree of the above-described suppression of the β 1,2-xylosyltransferase.

Preferably, the invention relates to recombinant human glycoproteins which have been produced in plant systems according to a method described above and whose peptide sequence comprises less than 50%, in particular less than 20%, particularly preferred 0%, of the β 1,2-bound xylose residues occurring in the proteins expressed in non-xylosyltransferase-reduced plant systems.

A particularly preferred embodiment relates to recombinant human glycoproteins for medical use which have been prepared in plant

systems according to a method described above and whose peptide sequence comprises less than 50%, in particular less than 20%, particularly preferred 0%, of the β 1,2-bound xylose residues occurring in the proteins expressed in non-xylosyltransferase-reduced plant systems.

The glycoproteins according to the invention may include other bound oligosaccharide units specific for plants, whereby - in the case of human glycoproteins - they differ from these natural glycoproteins. Nevertheless, by the glycoproteins according to the invention, a slighter immune reaction or no immune reaction at all, respectively, is triggered in the human body, since, as has already been explained in the introductory portion of the specification, the β 1,2-bound xylose residues, together with α 1,3-fucose residues, are the main cause for the immune reactions or cross immune reaction, respectively, to plant glycoproteins.

A further aspect comprises a pharmaceutical composition comprising the glycoproteins according to the invention. In addition to the glycoproteins of the invention, the pharmaceutical composition comprises further additions common for such compositions. These are, e.g., suitable diluting agents of various buffer contents (e.g. Tris-HCl, acetate, phosphate, pH and ionic strength), additives, such as tensides and solubilizers (e.g. Tween 80, Polysorbate 80), preservatives (e.g. Thimerosal, benzyl alcohol), adjuvants, antioxidants (e.g. ascorbic acid, sodium metabisulfite), emulsifiers, fillers (e.g. lactose, mannitol), covalent bonds of polymers, such as polyethylene glycol, to the protein, incorporation of the material in particulate compositions of polymeric compounds, such as polylactic acid, polyglycolic acid, etc. or in liposomes, auxiliary agents and/or carrier substances which are suitable in the respective treatment. Such compositions will influence the physical condition, stability, rate of in vivo liberation and rate of in vivo excretion of the glycoproteins of the invention.

The invention also provides a method of selecting DNA molecules which code for a β 1,2-xylosyltransferase, in a sample, wherein the labelled DNA molecules of the invention or partial sequences thereof, are added to the sample, which bind to the DNA molecules

that code for a β 1,2-xylosyltransferase. The hybridized DNA molecules can be detected, quantitated and selected. For the sample to contain single strand DNA with which the labelled DNA molecules can hybridize, the sample is denatured, e.g. by heating.

One possible way is to separate the DNA to be assayed, possibly after the addition of endonucleases, by gel electrophoresis on an agarose gel. After having been transferred to a membrane of nitrocellulose, the labelled DNA molecules according to the invention are admixed which hybridize to the corresponding homologous DNA molecule ("Southern blotting").

Another possible way consists in finding homologous genes from other species by PCR-dependent methods using specific and/or degenerated primers, derived from the sequence of the DNA molecule according to the invention.

Advantageously the labelled DNA molecules of the invention or partial sequences thereof are immobilized onto carrier matrices. The use of DNA microarrays ("gene chips") is a further possible way to find homologous genes or to study the expression level of homologous genes. To this end, DNA representing either the entire genomic gene sequence, the full-length cDNA sequence, parts of these sequences or any combination of partial sequences, is immobilized onto carrier matrices, in order that homologous genes, after adding the sample to the carrier matrices, hybridize with the labelled DNA molecules (for examples see e.g. Ferea T.L. & Brown, P.O., 1999, Current Opinion in Genetics & Development 9: 715-722 and references cited herein).

Preferably, the sample for the above-identified inventive method comprises genomic DNA of a plant organism. By this method, a large number of plants or other species is assayed in a very rapid and efficient manner for the presence of the β 1,2-xylosyltransferase gene. In this manner, it is respectively possible to select plants or individuals of other species which do not comprise this gene, or to suppress or completely block, respectively, the expression of the β 1,2-xylosyltransferase in such plants or other organisms which comprise this gene, by an above-described method of the invention, so that subsequently they may be

used for the transfection and production of (human) glycoproteins.

The invention also relates to DNA molecules which code for a β 1,2-xylosyltransferase which have been selected according to the three last-mentioned methods and subsequently have been isolated from the sample. These molecules can be used for further assays. They can be sequenced and in turn can be used as DNA probes for finding β 1,2-xylosyltransferases. These - labelled - DNA molecules will function for organisms, which are related to the organisms from which they have been isolated, more efficiently as probes than the DNA molecules of the invention.

A further aspect of the invention relates to a preparation of β 1,2-xylosyltransferase cloned according to the invention which comprises isoforms having pI values of between 6.0 and 9.0, in particular between 7.50 and 8.00. The pI values of a protein is that pH value at which its net charge is zero and is dependent on the amino acid sequence, the glycosylation pattern as well as on the spatial structure of the protein. The β 1,2-xylosyltransferase may comprise several isoforms which have a pI value in this range. The reason for the various isoforms of the transferase are, e.g., different glycosylations as well as limited proteolysis. The pI value of a protein can be determined by isoelectric focussing, which is known to the skilled artisan.

The main isoform of the enzyme has an apparent molecular weight of 60,2 kDa.

In particular, the preparation of the invention comprises an isoform having a pI value of 7.52.

The invention also relates to a method of preparing "plantified" carbohydrate units of human and other vertebrate glycoproteins or other glycoconjugates, wherein UDP-xylose as well as β 1,2-xylosyltransferase encoded by an above-described DNA molecule are added to a sample that comprises a carbohydrate unit or a glycoprotein, respectively, so that xylose in β 1,2-position is bound by the β 1,2-xylosyltransferase to the carbohydrate unit or to the glycoprotein, respectively. By the method according to the inven-

tion for cloning β 1,2-xylosyltransferase it is possible to produce large amounts of purified enzyme. To obtain a fully active transferase, suitable reaction conditions are provided.

The invention will be explained in more detail by way of the following examples and drawing figures to which, of course, it shall not be restricted. In detail, in the drawings,

Fig. 1 shows the amino acid sequence of soybean peptide 2 and 3 (patent WO99/29835; SEQ ID NO: 3 and 5), the homology between these peptides and a *A. thaliana* sequence as well as the DNA sequence of four primers 1-4;

Fig. 2 shows the cDNA sequence of β 1,2-xylosyltransferase including 226 nt of the 5'-untranslated region;

Fig. 3 shows the amino acid sequence of β 1,2-xylosyltransferase derived therefrom;

Figs. 4a, 4b and 4c show the alignment of *A. thaliana* β 1,2-xylosyltransferase cDNAs, one genomic DNA and one EST sequence;

Fig. 5 shows the alignment of amino acid sequences of β 1,2-xylosyltransferase derived from the cDNAs, from a genomic DNA and from a EST sequence;

Fig. 6 is a schematic representation of the β 1,2-xylosyltransferase as well as the PCR-products and the hydrophobicity of the amino acid residues;

Fig. 7 shows a comparison of the β 1,2-xylosyltransferase activity of insect cells transfected with the β 1,2-xylosyltransferase gene with that of a negative control;

Figs. 8a and 8b shows the structure of the acceptor substrate and product of the β 1,2-xylosyltransferase;

Fig. 9 shows mass spectra;

Fig. 10 shows the analysis of the β 1,2-xylosyltransferase product

by reversed-phase HPLC, and

Fig. 11 shows the alignment of the predicted amino acid sequence derived from the cDNA of the present application with the amino acid sequence of the β 1,2-xylosyltransferase purified from soybean.

Example 1:

RT-PCR and cDNA cloning

Primers for the amplification of the putative β 1,2-xylosyltransferase cDNA by RT-PCR were designed as follows: A BLASTP search of the DDBJ database using two soybean peptides (SEQ ID NO: 1 and 2; corresponding to SEQ ID NO: 3 and 5 in Fig. 4 in patent WO99/29835 A1; however, the C-terminal amino acids LG were omitted from SEQ ID NO: 5) (see Fig.1) showed one protein sequence derived from an Arabidopsis thaliana genomic DNA sequence (Acc. Nr. AB015479) with more than 80 % homology (SEQ ID NO: 3). Primers 3 (SEQ ID NO: 4) and 4 (SEQ ID NO: 5) were based on the A. thaliana sequence homologous to the soybean peptides 2 and 3. Analysis of the homologous genomic DNA sequence using Gene-Finder at the BCM Search Launcher resulted in one predicted protein. Primer 1 (SEQ ID NO: 6) was designed to include the start codon of the predicted protein, whereas primer 2 (SEQ ID NO: 7) contains the stop codon of the predicted protein.

The entire RNA was isolated from young leaves of Arabidopsis thaliana var Columbia using the TRIzol reagent (Life Technologies). The RNA was treated with DNase (Promega, RQ1 RNase Free DNase) to remove traces of genomic DNA. First-strand cDNA was synthesised from 1 μ g of total RNA at 42°C using oligo(dT) primers (Sigma) and AMV reverse transcriptase (Promega).

The first strand cDNA was subjected to a PCR, wherein different combinations of sense and antisense primers were used (illustrated in Fig. 6): The product of primer 3 and primer 4 was a DNA fragment with length of 174 bp (P1), the product of primer 1 and primer 2 was a 1605 bp (P2) DNA fragment, the product of primer 1 and primer 4 was a DNA fragment with length of 1525 bp (P3) and primer 3 and primer 4 produced a DNA of 254 bp (P4). For amplifi-

cation of the putative open reading frame primer 1 and primer 2 were used. A PCR reaction contained in a total volume of 50 μ l 0.2 μ mol of each primer, 0.05 mM dNTPs, 2 mM MgSO_4 , 20 mM Tris-HCl (pH 8.2 at 25°C), 10 mM KCl, 10 mM $(\text{NH}_4)_2\text{SO}_4$, 0.1 % Triton X-100, 5 μ g nuclease-free BSA and 2.5 units Pfu DNA polymerase from Promega. After a first denaturing step at 94°C for 2 min, 30 cycles of 1 min at 92°C, 40 sec at 53°C and 3 min and 30 sec at 72°C were performed. The last extension step was carried out at 72°C for 8 min. PCR products were subcloned into SmaI linearised and dephosphorylated puc19 vector, and sequenced: The sequences of the subcloned fragments were obtained by means of the dideoxynucleotide method (ABI PRISM Dye Termination Cycle Sequencing Ready reaction Kit and ABI PRISM 310 Genetic analyzer from Perkin Elmer). As a result of the RT-PCR three slightly different cDNA sequences were obtained. The sequence of cDNA 6 which has a size of 1605 bp (xt-Ath6; SEQ ID NO: 8) and codes for a protein of 534 amino acids having a molecular weight of 60.2 kDa and a theoretical pI value of 7.52 (see Fig. 3) is identical to the nucleotide sequence derived from the genomic clone after removing of two introns (xt-Athgen.seq). cDNA 9 shows 4 base pair changes compared to cDNA 6, whereas cDNA 16 shows 6 base pair changes compared to cDNA 6 (illustrated in Figs. 4a, 4b and 4c). Therefore the amino acid sequence derived from cDNA 9 comprises two changes compared to the amino acid sequence derived from cDNA 6 (SEQ ID NO: 8), and the amino acid sequence of cDNA 16 shows four changed residues (illustrated in Fig. 5).

Fig. 3 shows the cDNA-derived amino acid sequence (SEQ ID NO: 9) of the β 1,2-xylosyltransferase (xt-Ath6; SEQ ID NO: 8). Potential sites for the asparagine-bound glycosylation are at Asn51, Asn301 and Asn479.

Figs. 4a, 4b and 4c show the alignment of β 1,2-xylosyltransferase nucleotide sequences from the *A. thaliana* cDNA 6 (xt-Ath6; SEQ ID NO: 8), the *A. thaliana* cDNA 9 (xt-Ath9), the *A. thaliana* cDNA 16 (xt-Ath16), the *A. thaliana* genomic DNA sequence after removing of two introns (xt-Athgen), and from a *A. thaliana* EST sequence (xtAthEST). The dotted line stands for the consensus sequence; the dashed line for a gap.

The genomic sequence (xt-Athgen; Acc. No. AB015479, start codon at position 58185-58187, stop codon at position 60214-60216 of the genomic DNA) results from removing of two putative introns (intron 1: from position 58881 to 59116 of the genomic DNA; intron 2: from position 59268 to 59458 of the genomic DNA) using the splice site prediction server NetPlantGene. The *A. thaliana* EST sequence (xt-AthEST; Acc. No. AI994524) is the result of a database search using BLASTN.

Fig. 5 shows the alignment of amino acid sequences from β 1,2-xylosyltransferase derived from *A. thaliana* cDNA 6 (xt-Ath6; SEQ ID NO: 9), from *A. thaliana* cDNA 9 (xt-Ath9), from *A. thaliana* cDNA 16 (xt-Ath16), from the *A. thaliana* genomic sequence (xt-Athgen), and derived from a *A. thaliana* EST sequence (xt-AthEST). The dotted line stands for a consensus sequence; the dashed line stands for a gap.

In Fig. 6, the schematic predicted β 1,2-xylosyltransferase protein (top) and the derived hydrophobicity index using ProtScale, of the encoded protein (bottom) are illustrated, a positive hydrophobicity index meaning an increased hydrophobicity. Therebetween the sizes of the four above-indicated PCR products (P1-P4) are shown in relationship to the cDNA. "C" coding for the postulated cytoplasmic region, "T" for the postulated transmembrane region, and "G" for the postulated Golgi lumen catalytic region of the transferase. The analysis of the protein sequence by "TMPred" (from EMBnet,) gave an assumed transmembrane region from Ile11 to Phe29. The C-terminal region of the enzyme probably comprises the catalytic region and consequently should point into the lumen of the Golgi apparatus. According to this, this transferase seems to be a type II transmembrane protein like all the hitherto analysed glycosyltransferases which are involved in glycoprotein biosynthesis (Joziasse, 1992, Glycobiology 2, 271-277). The grey regions represent the position of the two peptides, the hexagons represent the potential N-glycosylation sites. A BLAST search in data banks accessible via NCBI showed only high homology to one other plant sequence (hybrid aspen, Acc. No. AI62640).

Example 2 :

Expression of recombinant β 1,2-xylosyltransferase in insect cells

The entire coding region of the assumed β 1,2-xylosyltransferase including cytoplasmatic and transmembrane region was removed from the puc19 vector by BamHI and EcoRI digestion and subcloned into BamHI / EcoRI digested and dephosphorylated baculovirus transfer vector pVL 1393 (PharMingen, San Diego, CA). Correct cloning was confirmed by sequencing using pVL1393 forward primer 5'-AACCATCTCGCAAATAAATAAGTA-3' (SEQ ID NO: 10) and pVL1393 reverse primer 5'-GTCGGGTTTAAACATTACGGATTTC-3' (SEQ ID NO: 11). To ensure a homologous recombination, 1 μ g of the transfer vector was co-transfected with 200 ng linear Baculo-Gold viral DNA (PharMingen, San Diego, CA) into 1×10^6 Sf-9 cells in IPL-41 Medium using Lipofectin (Life Technologies) according to the manufacturer's protocol. After an incubation of 5 days at 27° C, various volumes of the supernatant with the recombinant virus were used for infection of Sf-21 insect cells. Cells were incubated in IPL-41 medium supplemented with 5 % heat-inactivated fetal calf serum for 4 days at 27° C, then harvested and washed 2x with phosphate-buffered saline solution. The cells were resuspended and homogenised in the following buffer (1 ml per 10^7 cells): 100 mM MES buffer, pH 7.0, with 1 % Triton X-100, 1 mM DTT, 1 mM PMSF, 5 μ g/ml Leupeptin (Sigma), 5 μ g/ml E-64 (Serva) and incubated on ice for 30 min.

Example 3:

Assay for β 1,2-xylosyltransferase activity

The cell homogenates were assayed for β 1,2-xylosyltransferase activity. Negative controls were carried out with the same number of uninfected cells. The assay mixtures contained, in a total volume of 20 μ l, 13 μ l of homogenised cells, 2 nmol dabsylated GnGn hexapeptide or GnGn-pyridylamine as acceptor substrate (Fig. 8a), 1 mM UDP-xylose as donor substrate, 10 mM ATP, 20 mM MnCl₂ and 1 mM 2-acetamido-1,2-dideoxy-nojirimycin was included to prevent degradation of product by N-acetylhexosaminidase. The samples were incubated for 1 hour at 37° C and analysed by MALDI-TOF mass spectrometry.

Fig. 7 shows the measured enzyme activity of the recombinant β 1,2-xylosyltransferase as well as of the negative control. Grey

bars show the activity when GnGn hexapeptide was used as a substrate, whereas black bars indicate the use of GnGn-pyridylamin as a substrate. The enzyme activity of the cotransfected cells was 30x higher than that of the negative controls.

The structure of the acceptor substrate of β 1,2-xylosyltransferase is shown in Fig. 8a, and the postulated product in Fig. 8b, where R represents either a pyridylamine or dabsylated hexapeptide residue.

Example 4 :

Mass spectrometry of the xylosyltransferase product

Mass spectrometry was performed on a DYNAMO (BioAnalysis, Santa Fe, NM), a MALDITOF MS which is capable of dynamic extraction (synonym for late extraction). Two types of sample matrix preparations were used: dabsylated glycopeptides were dissolved in 5 % formic acid, and aliquots were applied to the target, air-dried, and covered with 1 % alpha-cyano-4-hydroxy cinnamic acid. Pyridylaminated glycans were diluted with water, applied to the target and air-dried. After addition of 2 % 2,5-dihydroxy benzoic acid, the samples were immediately dried by applying vacuum.

Fig. 9 shows the mass spectrum of these samples, (A) being the negative control: The main peak (S) shows the dabsyl-Val-Gly-Glu-(GlcNAc₆Man₃)Asn-Arg-Thr substrate, the calculated $[M+H]^+$ value being 2262.3. This substrate also appears as sodium addition product and as smaller ion which has been formed by fragmentation of the Azo function of the dabsyl group, at (S*). The peak at m/z = 2424.4 shows the incomplete de-galactosylation of the substrate. The mass spectrum (B) shows the sample with recombinant β 1,2-xylosyltransferase after incubation for 1 h at 37° C. The main peak (P), having a $[M+H]^+$ value of 2393.4, represents the xylosylated product.

Example 5 :

HPLC-analysis of the xylosyltransferase product

Xylosyltransferase assays were performed as described above under example 3, except that 10 nmol of GnGn-pyridylamine were used as

the acceptor substrate. After 4 h of incubation the sample was analyzed both by MALDI-TOF mass spectrometry and by reversed-phase HPLC to verify the structure of the product. The presumed product peak eluting slightly ahead of the substrate GnGn-PA was collected. By MALDI-TOF MS the product's mass was determined to be 1550.9 which is in good agreement with being GnGnX-PA. Upon digestion with β -N-acetylglucosaminidase from bovine kidney (in 50 mM sodium citrate buffer of pH 5.0 for 20 h at 37°C with 25 mU of enzyme), the glycan eluted with about the retention of MM. This is in keeping with published data on the retention of MM-PA and MMX-PA (Wilson & Altmann, 1998, *Glycoconj. J.* 15, 1055-1070). Further digestion with α -mannosidase from jack beans under the chosen conditions (20 h at 37°C with 50 mU of enzyme) resulted in the appearance of two new peaks. As the α -1,3-linked mannose is considerably more sensitive to mannosidase than the α -1,6-linked mannose, the peaks are assigned to 00X and MOX (in the order of elution). Indeed, MOX-pyridylamine prepared from bromelain by defucosylation with acid coeluted with the presumed MOX derived from the xylosyltransferase product. The fairly high shift of elution time due to the removal of the α -1,3-linked mannose residue is a strong indication of the β -mannose being substituted by xylose (Wilson & Altmann, 1998, *Glycoconj. J.* 15, 1055-1070; Altmann, 1998, *Glycoconj. J.* 15, 79-82).

Fig. 10 shows the analysis of the xylosyltransferase product by reversed-phase HPLC. (A) transferase incubation mixture; (B) isolated xylosyltransferase product; (C) isolated xylosyltransferase product after digestion with β -N-acetylglucosaminidase; (D) isolated xylosyltransferase product after further digestion with α -mannosidase. The assignments of peaks are as follows: 1, GnGn-PA; 2, GnGnX-PA; 3, MMX-PA; 4, MOX-PA; 5, 00X-PAA; 6, MO-PA (from trace of substrate in isolated product). For abbreviations of N-glycan structures see Wilson I.B.H. and Altmann, F., 1998, *Glycoconj. J.* 15, 1055-1077.

Fig. 11 shows the alignment of the predicted amino acid sequence according to the WO 99/29835 A1. This alignment shows that the amino acid sequence of the purified soybean enzyme corresponds only to amino acids 199-469 of the sequence derived from the cDNA according to the present invention. Furthermore, the predicted

amino acid sequence derived from the cDNA of the present application contains two insertions (corresponding to aa 375-382 and aa 425-429 of the predicted sequence) compared to the sequence of the purified soybean enzyme.

Claims:

1. A DNA molecule, characterized in that it comprises a sequence according to SEQ ID NO: 8 with an open reading frame from base pair 227 to base pair 1831, or is at least 50% homologous with the above sequence, or hybridizes with the above sequence under stringent conditions, or comprises a sequence which has degenerated to the above DNA sequence due to the genetic code, with the sequence coding for a plant protein having xylosyltransferase activity or being complementary thereto.
2. A DNA molecule according to claim 1, characterized in that it codes for a protein having β 1,2-xylosyltransferase activity.
3. A DNA molecule according to claims 1 or 2, characterized in that it is at least 70%, preferably at least 80%, particularly preferably at least 95% homologous with the sequence according to SEQ ID NO 8.
4. A DNA molecule according to any one of claims 1 to 3, characterized in that it comprises 1780 to 1880, particularly 1831 base pairs.
5. A DNA molecule according to any one of claims 1 to 4, characterized in that it is covalently associated with a detectable marker substance.
6. A DNA molecule according to any one of claims 1 to 5, characterized in that said DNA sequence comprises a deletion, insertion and/or substitution mutation.
7. A DNA molecule coding for a ribozyme, characterized in that it has two sequence sections, each of which has a length of at least 10 to 15 base pairs and which are complementary to the sequence sections of a DNA molecule according to any one of claims 1 to 5 so that said ribozyme complexes and cuts the mRNA transcribed by a natural β 1,2-xylosyltransferase DNA molecule.
8. A biologically functional vector, characterized in that it

- comprises a DNA molecule according to any one of claims 1 to 5.
9. A biologically functional vector, characterized in that it comprises a DNA molecule according to any one of claims 1 to 5 being inversely orientated with respect to the promotor.
10. A biologically functional vector, characterized in that it comprises a DNA molecule according to claims 6 or 7.
11. A method of preparing a cDNA comprising a DNA molecule according to any one of claims 1 to 4, characterized in that RNA is isolated from plant cells, particularly from leaf cells, and with said RNA a reverse transcription is effected after the addition of a reverse transcriptase and primers.
12. A method of cloning a β 1,2-xylosyltransferase, characterized in that a DNA molecule according to any one of claims 1 to 4 is cloned into a vector subsequently transfected into a host cell or a host, with cell lines being obtained by means of selection and amplification of transfected host cells, which cell lines express the active β 1,2-xylosyltransferase.
13. A method of preparing recombinant host cells, particularly plant cells, or plants, wherein the production of β 1,2-xylosyltransferase is suppressed or completely stopped, characterized in that at least one of the vectors according to one of the claims 8 to 10 is inserted into said host cell or plant, respectively.
14. A method of preparing recombinant host cells, particularly plant cells or plants, respectively, characterized in that the DNA molecule according to claim 6 is inserted into the genome of said host cell or plant, respectively, at the position of the non-mutated, homologous sequence.
15. Recombinant plants or plant cells, characterized in that they are prepared according to a method according to claims 13 or 14 and that their β 1,2-xylosyltransferase production is suppressed or completely stopped.
16. A PNA molecule, characterized in that it comprises a base se-

quence complementary to the sequence of a DNA molecule according to any one of claims 1 to 4.

17. A PNA molecule, characterized in that it comprises a base sequence corresponding to the sequence of a DNA molecule according to any one of claims 1 to 4.

18. A method of producing plants or plant cells, respectively, particularly plant cells having blocked expression of β 1,2-xylosyltransferase at the transcription or translation level, characterized in that PNA molecules according to claims 16 or 17 are inserted into the cells.

19. A method of producing recombinant glycoproteins, characterized in that the system according to claim 15 or plants or cells, respectively, which are prepared according to a method according to claim 18, is (are) transfected with the gene that expresses the glycoprotein so that the recombinant glycoproteins are expressed.

20. A method of producing recombinant human glycoproteins, characterized in that the system according to claim 15 or plants or cells, respectively, which are prepared according to a method according to claim 18, is (are) transfected with the gene that expresses the glycoprotein so that the recombinant glycoproteins are expressed.

21. A method of producing recombinant human glycoproteins for medical use, characterized in that the system according to claim 15 or plants or cells, respectively, which are prepared according to a method according to claim 18, is (are) transfected with the gene that expresses the glycoprotein so that the recombinant glycoproteins are expressed.

22. Recombinant glycoproteins, characterized in that they are prepared according to the method according to claim 19 in plant systems and that their peptide sequence has less than 50%, particularly less than 20%, particularly preferably 0% of β 1,2-bound xylose residues present in proteins expressed in non-xylosyltransferase reduced plant systems.

23. Recombinant human glycoproteins, characterized in that they are prepared according to the method according to claim 20 in plant systems and that their peptide sequence has less than 50%, particularly less than 20%, particularly preferably 0% of β 1,2-bound xylose residues present in proteins expressed in non-xylosyltransferase reduced plant systems.
24. Recombinant human glycoproteins for medical use, characterized in that they are prepared according to the method according to claim 21 in plant systems and that their peptide sequence has less than 50%, particularly less than 20%, particularly preferably 0% of β 1,2-bound xylose residues present in proteins expressed in non-xylosyltransferase reduced plant systems.
25. A pharmaceutical composition, characterized in that it comprises recombinant glycoproteins according to any one of claims 22 to 24.
26. A method of selecting DNA molecules coding for a β 1,2-xylosyltransferase, in a sample, characterized in that DNA molecules according to claim 5 are added to said sample, which molecules bind to the DNA molecules coding for a β 1,2-xylosyltransferase.
27. A method according to claim 26, characterized in that said sample comprises genomic DNA of a plant or non-vertebrate animal organism.
28. DNA molecules coding for a β 1,2-xylosyltransferase, characterized in that they are selected according to the method according to claims 26 or 27 and are subsequently isolated from the sample.
29. A preparation of β 1,2-xylosyltransferase cloned according to a method according to claim 12, characterized in that it has isoforms having pI values of between 6.0 and 9.0, particularly between 7.50 and 8.00.
30. A preparation according to claim 29, characterized in that it has an isoform having a pI value of 7.52.

31. A method of preparing plantified carbohydrate units of human and other vertebrate glycoproteins, characterized in that to a sample comprising a carbohydrate unit or any glycoconjugate or a glycoprotein, respectively, are added UDP-xylose and β 1,2-xylosyltransferase coded by a DNA molecule according to any one of claims 1 to 5 so that xylose is bound to said carbohydrate unit or glycoconjugate or said glycoprotein, respectively, at the β 1,2-position by said β 1,2-xylosyltransferase.

32. The use of DNA according to any one of claims 1 to 6 or partial sequences or of combinations of partial sequences for immobilisation on DNA microarrays, e.g. for finding homologous sequences or for expression studies in plants or non-vertebrate animals.

KP/Se

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Peptide 3 from patent WO9929835A1 SQVQAIHDASVIIGAHGAGLTHIVSAL

Peptide 2 from patent WO9929835A1¹ GLEYHAIN

Soybean: SQVQAIHDASVIIGAHGAGLTHIVSAL—————GLEYHAIN
 QV AI DASVIIGAHGAGLTHIVSA GLEYHA
A.thaliana: DQVRAIQDASVIIGAHGAGLTHIVSATPNTTIFELISVEFQRPHELLAKWKGLEYPHAMH

Primer 1 5'-ATGAGTAAACGGAATCCGAAG-3'

Primer 2 5'-TTAGCAGCCAAGGCTCTTCAT-3'

Primer 3 5'-GATCAAGTCCGAGCCATTCAA-3'

Primer 4 5'-CGCGTGATACTCCAATCCTTT-3'

¹The C-terminal amino acids LG were omitted

Fig. 1

AAATCTGCAGACTCTCAAAATTCGGATTCATCTTATGAAGAACAA 46
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TCAAATTCCTCGCTCTCTCTTCAAAACCGCAAATCAAGGGAACGAGAGACGAGAGAGAGAG 226
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CTCTTTCTCATCATCTACTTCTGTTTTCACCTCATCGTCGTTTTCACCGGAGCAGTCACAG 346
CCTCCTCATATATACCACGTTTCAGTGAATAACCAATCGCGGATTCAGAAACCGTGGCCG 406
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AAGTTAGAGGAAGTTATGGGGAGGAAAGAGGAGGAGGCTTCTCGCGTTTTCGACAGGT 706
GCGTTTGAGGTAGCGGAAGAGGTTTCTTCACGGTTAGGTTTTAAGAGACACCGTCGTTTT 766
GGTGGAGGAGAAGGAGGTAGTGCAGTTTCTCGCGGCTGGTGAATGATGAGATGTTGAAT 826
GAATATATGCAAGAAGGTGGAATTGATAGACATACAATGAGAGATTGGTTGCTTCGATT 886
CGTGCTGTTGATACCAATGATTTCGTTTGTGAAGAGTGGGTGGAGGAACCGACCTTGCTT 946
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TGGAAAGGATTGGAGTATCACGCGATGCATCTGGGGAACCTCAGAGCGGAACCAACGGCT 1786
GTGATTGAGAAGTTAACGGAGATCATGAAGAGCCTTGCTGCTAA 1831

Fig. 2

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130 140 150 160 170 180
CEGRNLRMPDRIVMSRGGEKLEEVMGREEELPAFRQGAFEVAEEVSSRLGFKRHRFF

190 200 210 220 230 240
GGGEGGSAVSRRLVNDEMLNEYMQEGGIDRHTMRDLVASIRAVDTNDFVCEEVVEEPTLL

250 260 270 280 290 300
VTRFEYANLFHTVTDWYSAYVSSRVTLGNRPHVVPVDGHCTTQLEETWTALFSGIRYAK

310 320 330 340 350 360
NFTKPVCFRHAISPLGYETALFKGLSGEIDCKGDSAHNLWQNPDDKRTARISEFGEMIR

370 380 390 400 410 420
AAFGLPVNRHRSLEKPLSSSSSSASVYNVLFVRREDYLAHPRHGCKVQSRLINEEEVFDS

430 440 450 460 470 480
LHHWVATGSTGLTKCGINLVNGLLAHMSMKDQVRAIQDASVIIGAHGAGLTHIVSATPNT

490 500 510 520 530
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Fig. 3

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xt-Ath16.seq : ..... : 80
xt-Athgen.seq : ..... : 80
xt-AthEST.seq : ..... : 80
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xt-Ath9.seq : ..... : 160
xt-Ath16.seq : ..... : 160
xt-Athgen.seq : ..... : 160
xt-AthEST.seq : ..... : 160
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xt-Ath6.seq : CGATTGAGAAACCGTGGCCGATCTTACGTTCTTACCTGCCATGACCCGCCGAGAGGAATCTACCAACTGGCTCTCTG : 240
xt-Ath9.seq : ..... : 240
xt-Ath16.seq : ..... : 240
xt-Athgen.seq : ..... : 240
xt-AthEST.seq : ..... : 240
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xt-Ath6.seq : GAAAGTTACTTCCGGATGGATTACAAAGAGAGATTGACTTCTTAAAGCGAGGATTGGAGGAGGAGGAGGAGGCTG : 320
xt-Ath9.seq : ..... : 320
xt-Ath16.seq : ..... : 320
xt-Athgen.seq : ..... : 320
xt-AthEST.seq : ..... : 320
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xt-Ath9.seq : ..... : 400
xt-Ath16.seq : ..... : 400
xt-Athgen.seq : ..... : 400
xt-AthEST.seq : ..... : 400
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xt-Ath6.seq : TTATGTCGAGAGGAGGTGAGAAATTAGAGGAAGTTATGGGGAGCAAGAGGAGGAGGACTTCTGCGTTTCGACAAAGT : 480
xt-Ath9.seq : ..... : 480
xt-Ath16.seq : ..... : 480
xt-Athgen.seq : ..... : 480
xt-AthEST.seq : ..... : 480
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xt-Ath6.seq : GCGTTTGAGGTACCGGAGAGAGGTTTCTTCACGGTTAGGTTTAAAGACACCCGTCGTTTGGTGAGGAGGAGGAGGTAG : 560
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Fig. 4a

```

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xt-Athgen.seq : ..... : 640
xt-AthEST.seq : ..... : 640
-

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xt-Ath9.seq : ..... : 720
xt-Ath16.seq : ..... : 720
xt-Athgen.seq : ..... : 720
xt-AthEST.seq : ..... : 720
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xt-Ath6.seq : GTCACTAGATTCCAGTACGCAAAATCTCTTCCATACCTGTGACAGATTGGTATATGCTCTATGTTTCTCTAGAGTCACCGG : 800
xt-Ath9.seq : ..... : 800
xt-Ath16.seq : ..... : 800
xt-Athgen.seq : ..... : 800
xt-AthEST.seq : ..... : 152

xt-Ath6.seq : TTTGCTTAATGAGCCTCACGTTGTTTTCTGTTGACGGACACTGCACGACCGAGCTAGAGAAGAACATGGACAGCTTTGTTT : 880
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xt-Ath16.seq : ..... : 880
xt-Athgen.seq : ..... : 880
xt-AthEST.seq : ..... : 232

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xt-Athgen.seq : ..... : 960
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xt-Ath16.seq : ..... : 1040
xt-Athgen.seq : ..... : 1040
xt-AthEST.seq : .....G..... : 1040
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xt-Ath6.seq : AAGCACTCCGAGGATATCAGAGTTTGGTGAATGATCAGACGAGCTTTGGGCTTGCCCTGTCAATGACACCGGCTCATTA : 1120
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xt-Ath16.seq : ..... : 1120
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```

Fig. 4b

```

xt-Ath6.seq : AAAAGCGCGTATCATCATCATCATCAGCGCTCACTTATATGTTCTTTTGTCGCGCGTGAGAGATTACTTAGCCCAT : 1200
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xt-Ath16.seq : ..... : 1200
xt-Athgen.seq : ..... : 1200
xt-AthEST.seq : G..... : 482

xt-Ath6.seq : CCTCTCATGCGCGTAAAGTCCAGTCTCGCGCTCATCAATGAGGAAGTGTGACATGGTTGCATCATTTGGGTTGCAAC : 1280
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xt-Ath16.seq : ..... : 1280
xt-Athgen.seq : ..... : 1280
xt-AthEST.seq : ..... : -

xt-Ath6.seq : TGGGTCCACCGGTCTGACCAATGCGGGATTAACTTGTGAATGGCTTGCTTGCACACATGTCAATGAAAGATCAAGTCC : 1360
xt-Ath9.seq : ..... : 1360
xt-Ath16.seq : ..... : 1360
xt-Athgen.seq : ..... : 1360
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xt-Ath16.seq : ..... : 1440
xt-Athgen.seq : ..... : 1440
xt-AthEST.seq : ..... : -

xt-Ath6.seq : ACGATATTGAGATAATAAGCGCTGAGCTTCAGAGACCTCATTTGAGCTTATAGCTAAAGTGGAAAGGATTGCACTATCA : 1520
xt-Ath9.seq : ..... : 1520
xt-Ath16.seq : ..... : 1520
xt-Athgen.seq : ..... : 1520
xt-AthEST.seq : ..... : 1520

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xt-Ath16.seq : ..... : 1600
xt-Athgen.seq : ..... : 1600
xt-AthEST.seq : ..... : 1600

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xt-Athgen.seq : ..... : 1605
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Fig. 4c

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xt-Ath16.seq : ..... : 80
xt-Athgen.seq : ..... : 80
xt-AthEST.seq : ..... : -

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xt-Ath9.seq : ..... : 160
xt-Ath16.seq : ..... : 160
xt-Athgen.seq : ..... : 160
xt-AthEST.seq : ..... : -

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xt-Ath16.seq : ..... : 240
xt-Athgen.seq : ..... : 240
xt-AthEST.seq : ..... : 24

xt-Ath6.seq : VTRFETANLFRHTVDWYSAYVSSRVLTGLPWRPWPVVDORCTTOLEETWTALFSGIPIAKNFTKPCVRMAILSPLOYET : 320
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xt-Athgen.seq : ..... : 320
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xt-Ath16.seq : ..... : 400
xt-Athgen.seq : ..... : 400
xt-AthEST.seq : ..... : 160

xt-Ath6.seq : PEHGGVQVSRLINEEYVFDLSLHEWVATGSTLTGCGEINLVNGLAHNSKEDQVRIQDSAVLIGAGAGLTHIVSATPNT : 480
xt-Ath9.seq : ..... : 480
xt-Ath16.seq : ..... : 480
xt-Athgen.seq : ..... : 480
xt-AthEST.seq : ..... : -

xt-Ath6.seq : TIFEIISVEFORPHFELIANWGLETHAWRLANSRAEPTAVIEKLTINKSLGC : 534
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Fig. 5

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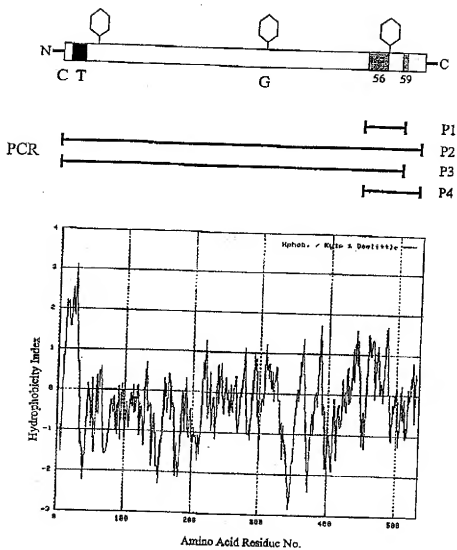


Fig. 6

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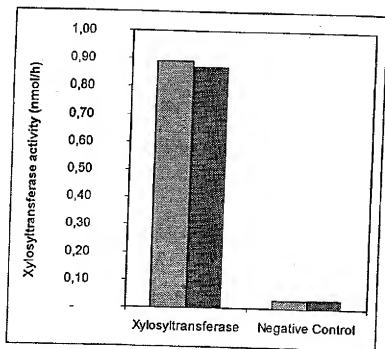


Fig. 7

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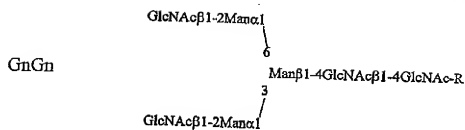


Fig. 8a

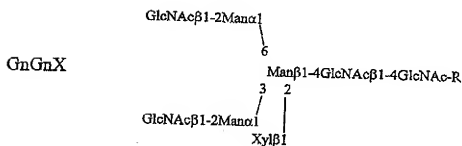


Fig. 8b

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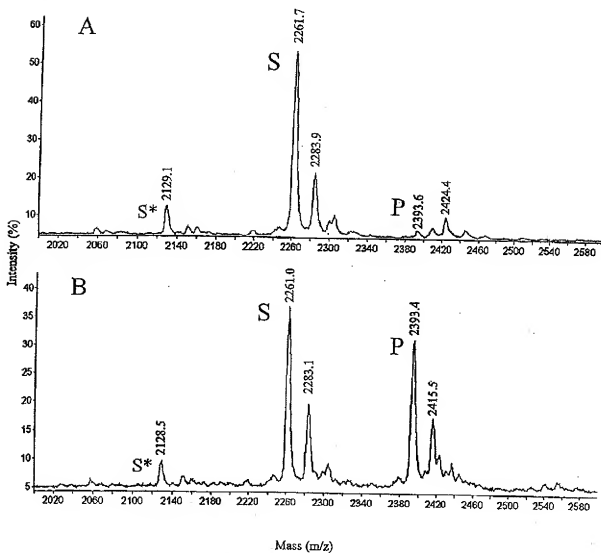


Fig. 9

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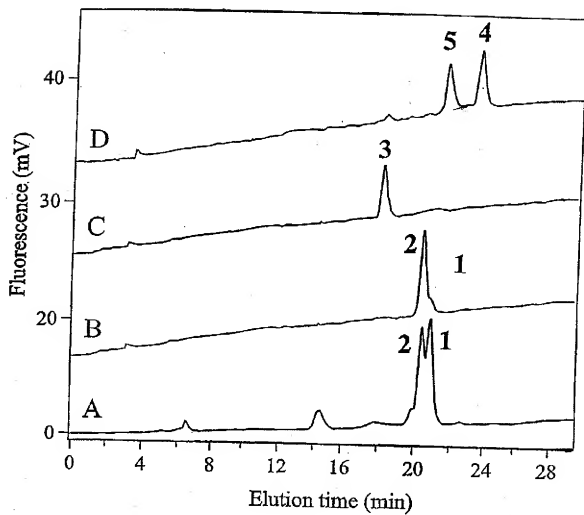


Fig. 10

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25

30

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Ser Phe Ser Pro Glu Gln Ser Gln Pro Pro His Ile Tyr His Val Ser
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Val Asn Asn Gln Ser Ala Ile Gln Lys Pro Trp Pro Ile Leu Pro Ser
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Tyr Leu Pro Trp Thr Pro Pro Gln Arg Asn Leu Pro Thr Gly Ser Cys
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Glu Gly Tyr Phe Gly Asn Gly Phe Thr Lys Arg Val Asp Phe Leu Lys
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Pro Arg Ile Gly Gly Gly Gly Glu Gly Ser Trp Phe Arg Cys Phe Tyr
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Ser Glu Thr Leu Gln Ser Ser Ile Cys Glu Gly Arg Asn Leu Arg Met
 115 120 125

Val Pro Asp Arg Ile Val Met Ser Arg Gly Gly Glu Lys Leu Glu Glu
 130 135 140

Val Met Gly Arg Lys Glu Glu Glu Leu Pro Ala Phe Arg Gln Gly
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Ala Phe Glu Val Ala Glu Glu Val Ser Ser Arg Leu Gly Phe Lys Arg
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His Arg Arg Phe Gly Gly Gly Glu Gly Gly Ser Ala Val Ser Arg Arg
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Leu Val Asn Asp Glu Met Leu Asn Glu Tyr Met Gln Glu Gly Gly Ile
 195 200 205

Asp Arg His Thr Met Arg Asp Leu Val Ala Ser Ile Arg Ala Val Asp
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Thr Asn Asp Phe Val Cys Glu Glu Trp Val Glu Glu Pro Thr Leu Leu
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Val Thr Arg Phe Glu Tyr Ala Asn Leu Phe His Thr Val Thr Asp Trp
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Tyr Ser Ala Tyr Val Ser Ser Arg Val Thr Gly Leu Pro Asn Arg Pro
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 His Val Val Phe Val Asp Gly His Cys Thr Thr Gln Leu Glu Thr
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 Ala Leu Phe Lys Gly Leu Ser Gly Glu Ile Asp Cys Lys Gly Asp Ser
 325 330 335
 Ala His Asn Leu Trp Gln Asn Pro Asp Asp Lys Arg Thr Ala Arg Ile
 340 345 350
 Ser Glu Phe Gly Glu Met Ile Arg Ala Ala Phe Gly Leu Pro Val Asn
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 Arg His Arg Ser Leu Glu Lys Pro Leu Ser Ser Ser Ser Ser Ala
 370 375 380
 Ser Val Tyr Asn Val Leu Phe Val Arg Arg Glu Asp Tyr Leu Ala His
 385 390 395 400
 Pro Arg His Gly Gly Lys Val Gln Ser Arg Leu Ile Asn Glu Glu Glu
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 Val Phe Asp Ser Leu His His Trp Val Ala Thr Gly Ser Thr Gly Leu
 420 425 430
 Thr Lys Cys Gly Ile Asn Leu Val Asn Gly Leu Leu Ala His Met Ser
 435 440 445
 Met Lys Asp Gln Val Arg Ala Ile Gln Asp Ala Ser Val Ile Ile Gly
 450 455 460
 Ala His Gly Ala Gly Leu Thr His Ile Val Ser Ala Thr Pro Asn Thr
 465 470 475 480
 Thr Ile Phe Glu Ile Ile Ser Val Glu Phe Gln Arg Pro His Phe Glu
 485 490 495
 Leu Ile Ala Lys Trp Lys Gly Leu Glu Tyr His Ala Met His Leu Ala
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<223> Description of Artificial Sequence:primer

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24

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP-01/02352

A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C12N15/54 C12N15/82 C12N9/10 C12P21/02 A01H5/00 C12N5/10 C12N5/11		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 7 C12N C12P A01H		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practical, search terms used) EMBL, EPO-Internal, WPI Data, BIOSIS, CHEM ABS Data, PAJ		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 29835 A (UNIV ARKANSAS) 17 June 1999 (1999-06-17) cited in the application page 3, line 25 - page 4, line 22; claims; figure 10; table 4 page 35, line 22 - line 29 ---	1-6, 8-15, 19-21, 26-31
X	DATABASE EM_ESTA [Online] EMBL; Accession Number: A1994524, 9 September 1999 (1999-09-09) CHEN, J. ET AL: "Arabidopsis thaliana Gene Expression MicroArray" XP002173737 cited in the application Nucleotides 1-482 --- -/--	1,3,6,32
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C.		
<input checked="" type="checkbox"/> Patent family members are listed in annex.		
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later documents published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "S" document member of the same patent family		
Date of the actual completion of the international search 8 August 2001		Date of mailing of the international search report 13. 08. 01
Name and mailing address of the ISA European Patent Office, P.B. 5018 Patentkan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 apo nl, Fax: (+31-70) 340-3016		Authorized officer Madruga, J

Form PCT/ISA210 (secret, 01/97) (July 1992)

INTERNATIONAL SEARCH REPORT

Int. l. Application No

PCT/EP. 01/02352

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EM_PL [Online] EMBL; Accession Number: AB015479, 19 June 1998 (1998-06-19) NAKAMURA, Y.: "Arabidopsis thaliana genomic DNA" XP002173738 cited in the application Nucleotides 57959-58880 ---	1,3,6
X	ZENG Y ET AL: "PURIFICATION AND SPECIFICITY OF BETAL,2-XYLOSYLTRANSFERASE, AN ENZYME THAT CONTRIBUTES TO THE ALLERGENICITY OF SOME PLANT PROTEINS" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 272, no. 50, 12 December 1997 (1997-12-12), pages 31340-31347, XP002916555 ISSN: 0021-9258 the whole document ---	1,2
P,X	EP 1 033 405 A (CERES INC) 6 September 2000 (2000-09-06) SEQ ID No: 77277 ---	1,3,6
E	WO 01 29242 A (MONSANTO CO) 26 April 2001 (2001-04-26) page 75 -page 77; example 4 ---	1-21, 26-32
P,X	STRASSER R ET AL: "Molecular cloning and functional expression of betal,2-xylosyltransferase cDNA from Arabidopsis thaliana." FEBS LETTERS, vol. 472, no. 1, 21 April 2000 (2000-04-21), pages 105-108, XP002173735 ISSN: 0014-5793 the whole document ---	1-6
P,X	DATABASE EM_PL [Online] EMBL; Accession Number: ATH277603, 28 April 2000 (2000-04-28) BAKKER H: "Arabidopsis cDNA for beta 1, 2-xylosyltransferase" XP002173735 Nucleotides 1-1739 ---	1-6

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INTERNATIONAL SEARCH REPORT

International Application No.

PCT/EP-01/02352

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>LEROUGE P ET AL: "N-glycoprotein biosynthesis in plants: recent developments and future trends" PLANT MOLECULAR BIOLOGY, NIJHOFF PUBLISHERS, DORDRECHT, NL, vol. 38, 1998, pages 31-48, XP002140796 ISSN: 0167-4412 cited in the application the whole document</p> <p>---</p>	12-21, 26-32
A	<p>JENKINS N ET AL: "Getting the glycosylation right: implications for the biotechnology Industry" NATURE BIOTECHNOLOGY, NATURE PUBLISHING, US, vol. 14, no. 8, August 1996 (1996-08), pages 975-981, XP002133654 ISSN: 1087-0156 page 976, column 1, line 1 - line 8</p> <p>---</p>	12-21, 26-32
A	<p>RUAN Y ET AL: "TOWARDS ARABIDOPSIS GENOME ANALYSIS: MONITORING EXPRESSION PROFILES OF 1400 GENES USING CDNA MICROARRAYS" PLANT JOURNAL, BLACKWELL SCIENTIFIC PUBLICATIONS, OXFORD, GB, vol. 15, no. 6, September 1998 (1998-09), pages 821-833, XP000960486 ISSN: 0960-7412 the whole document</p> <p>-----</p>	32

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 01/02352**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 22-25
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 22-25

Present claims 22-25 relate to an extremely large number of possible products, namely glycoproteins having less than 50% beta 1, 2-bond xylose residues. In fact, these claims contain so many options, that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. In fact, any human recombinant glycoprotein not containing xylose residues (independently of how it is produced) will fall within the scope of these claims. Consequently, no search has been carried out for subject-matter of claims 22-25.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP. 01/02352

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9929835 A	17-06-1999	AU 1808699 A US 6168937 B	28-06-1999 02-01-2001
EP 1033405 A	06-09-2000	NONE	
WO 0129242 A	26-04-2001	NONE	